

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.

Application Serial Number: 09/518,763C
Source: /FW/b
Date Processed by STIC: 4/23/2002

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RAW SEQUENCE LISTING

DATE: 04/28/2008

PATENT APPLICATION: US/09/518,763C

TIME: 10:34:27

Input Set : N:\AMC\US09518763C.raw

Output Set: N:\CRF4\03192008\I518763C.raw

1 <110> APPLICANT: Blissard, Gary W.
 2 Granados, Robert R.
 3 Lin, Guangyun
 4 <120> TITLE OF INVENTION: STABLE CELL LINES RESISTANT TO APOPTOSIS AND NUTRIENT
 5 STRESS AND METHODS OF MAKING SAME
 6 <130> FILE REFERENCE: BTI44
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/518,763C
 8 <141> CURRENT FILING DATE: 2000-03-03
 9 <160> NUMBER OF SEQ ID NOS: 11
 10 <170> SOFTWARE: PatentIn Ver. 3.1
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 900
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Autographa californica nucleopolyhedrovirus
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (1)..(897)
 19 <300> PUBLICATION INFORMATION:
 20 <301> AUTHORS: Ayres, Martin D.
 21 Howard, Stephen C.
 22 Kuzio, John
 23 Lopez-Ferber, Miguel
 24 Possee, Robert D.
 25 <302> TITLE: The Complete DNA Sequence of Autographa californica
 26 Nuclear Polyhedrosis Virus
 27 <303> JOURNAL: Virology
 28 <304> VOLUME: 202
 29 <305> ISSUE: 2
 30 <306> PAGES: 586-605
 31 <307> DATE: 1994
 32 <308> DATABASE ACCESSION NO: L22858
 33 <309> DATABASE ENTRY DATE: 1999-03-08
 34 <313> RELEVANT RESIDUES: 116492 TO 117391
 35 <400> SEQUENCE: 1
 36 atg tgt gta att ttt ccg gta gaa atc gac gtg tcc cag acg att att 48
 37 Met Cys Val Ile Phe Pro Val Glu Ile Asp Val Ser Gln Thr Ile Ile
 38 1 5 10 15
 39 cga gat tgt cag gtg gac aaa caa acc aga gag ttg gtg tac att aac 96
 40 Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn
 41 20 25 30
 42 aag att atg aac acg caa ttg aca aaa ccc gtt ctc atg atg ttt aac 144
 43 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn
 44 35 40 45

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45 att tcg ggt cct ata cga agc gtt acg cgc aag aac aac aat ttg cgc 192
46 Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg
47 50 55 60
48 gac aga ata aaa tca aaa gtc gat gaa caa ttt gat caa cta gaa cgc 240
49 Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg
50 65 70 75 80
51 gat tac agc gat caa atg gat gga ttc cac gat agc atc aag tat ttt 288
52 Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe
53 85 90 95
54 aaa gat gaa cac tat tcg gta agt tgc caa aat ggc agc gtg ttg aaa 336
55 Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
56 100 105 110
57 agc aag ttt gct aaa att tta aag agt cat gat tat acc gat aaa aag 384
58 Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
59 115 120 125
60 tct att gaa gct tac gag aaa tac tgt ttg ccc aaa ttg gtc gac gaa 432
61 Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
62 130 135 140
63 cgc aac gac tac tac gtg gcg gta tgc gtg ttg aag ccg gga ttt gag 480
64 Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
65 145 150 155 160
66 aac ggc agc aac caa gtg cta tct ttc gag tac aac ccg att ggt aac 528
67 Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
68 165 170 175
69 aaa gtt att gtg ccg ttt gct cac gaa att aac gac acg gga ctt tac 576
70 Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
71 180 185 190
72 gag tac gac gtc gta gct tac gtg gac agt gtg cag ttt gat ggc gaa 624
73 Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
74 195 200 205
75 caa ttt gaa gag ttt gtg cag agt tta ata ttg ccg tcg tcg ttc aaa 672
76 Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
77 210 215 220
78 aat tcg gaa aag gtt tta tat tac aac gaa gcg tcg aaa aac aaa agc 720
79 Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
80 225 230 235 240
81 atg atc tac aag gct tta gag ttt act aca gaa tcg agc tgg ggc aaa 768
82 Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
83 245 250 255
84 tcc gaa aag tat aat tgg aaa att ttt tgt aac ggt ttt att tat gat 816
85 Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
86 260 265 270
87 aaa aaa tca aaa gtg ttg tat gtt aaa ttg cac aat gta act agt gca 864
88 Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala
89 275 280 285
90 ctc aac aaa aat gta ata tta aac aca att aaa taa 900
91 Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys
92 290 295
94 <210> SEQ ID NO: 2

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95 <211> LENGTH: 299
96 <212> TYPE: PRT
97 <213> ORGANISM: Autographa californica nucleopolyhedrovirus
98 <400> SEQUENCE: 2
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100      1           5           10           15
101   Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn
102      20           25           30
103   Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn
104      35           40           45
105   Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg
106      50           55           60
107   Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg
108      65           70           75           80
109   Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe
110      85           90           95
111   Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
112      100          105          110
113   Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
114      115          120          125
115   Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
116      130          135          140
117   Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
118      145          150          155          160
119   Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
120      165          170          175
121   Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
122      180          185          190
123   Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
124      195          200          205
125   Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
126      210          215          220
127   Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
128      225          230          235          240
129   Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
130      245          250          255
131   Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
132      260          265          270
133   Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala
134      275          280          285
135   Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys
136      290          295
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 38
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence:
144   oligonucleotide primer

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145 <400> SEQUENCE: 3
146      ctagaagttg gaaagatgcc agcggctggt cgtaatag      38
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149 <211> LENGTH: 38
150 <212> TYPE: DNA
151 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence:
154      oligonucleotide primer
155 <400> SEQUENCE: 4
156      ctagctatta cgaccagccg ctggcatctt tccaactt      38
158 <210> SEQ ID NO: 5
159 <211> LENGTH: 30
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of Artificial Sequence: p35upEcoRI
164      primer
165 <400> SEQUENCE: 5
166      cagaattcat gtgtgtaatt tttccggtag      30
168 <210> SEQ ID NO: 6
169 <211> LENGTH: 33
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: p35lowXbaI-NO
174      stop primer
175 <400> SEQUENCE: 6
176      ttttgcctca gatttaattg tgtttaatat tac      33
178 <210> SEQ ID NO: 7
179 <211> LENGTH: 35
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence:
184      p35lowXbaI-Stop primer
185 <400> SEQUENCE: 7
186      aatgctctag attatttaat tgtgtttaat attac      35
188 <210> SEQ ID NO: 8
189 <211> LENGTH: 15
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence:
194      p166-p35 linker DNA
195 <400> SEQUENCE: 8
196      ttaaacacaa ttaaa      15
198 <210> SEQ ID NO: 9
199 <211> LENGTH: 5

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200 <212> TYPE: PRT
201 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence:
204     p166-p35 linker polypeptide
205 <400> SEQUENCE: 9
206     Leu Asn Thr Ile Lys
207         1             5
209 <210> SEQ ID NO: 10
210 <211> LENGTH: 54
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence:
215     p166-p35-AcV5 linker DNA
216 <400> SEQUENCE: 10
217     ttaaacacaa ttaaattctag aagttggaaa gatgccagcg gctgggtcgta atag      54
219 <210> SEQ ID NO: 11
220 <211> LENGTH: 16
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence:
225     p166-p35-AcV5 linker polypeptide
226 <400> SEQUENCE: 11
227     Leu Asn Thr Ile Lys Ser Arg Ser Trp Lys Asp Ala Ser Gly Trp Ser
228         1             5             10             15

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VERIFICATION SUMMARY

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L:7 M:270 C: Current Application Number differs, Wrong Format